SEQUENCE LISTING

<110> Seisi Kato Yamaguchi Kimura Shingo Sekine Kouju Kamata

<120> HUMAN GALECTIN-9-LIKE PROTEINS AND cDNAs PROTEINS



<130> GIN-6707CPUS

<140> 09/485,951

<141> 2000-02-17

<150> 9-226468

<151> 1997-08-22

<150> PCT/JP98/03670

<151> 1998-08-19

<160> 11

<170> PatentIn Ver. 2.0

<210> 1

<211> 32

<212> PRT

<213> Homo sapiens

<400> 1

Asn Pro Arg Thr Val Pro Val Gln Pro Ala Phe Ser Thr Val Pro Phe

Ser Gln Pro Val Cys Phe Pro Pro Arg Pro Arg Gly Arg Arg Gln Lys

<210> 2

<211> 355

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro Ala Val Pro

Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu Gln Ile Thr 20

Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn

Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro



RECEIVED

JAN 12 2001

TECH CENTER 1600/2900

50 55 60

Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly 70 Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val 105 Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe 115 120 His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr 135 Ile Ser Phe Gln Asn Pro Arg Thr Val Pro Val Gln Pro Ala Phe Ser 145 150 155 Thr Val Pro Phe Ser Gln Pro Val Cys Phe Pro Pro Arg Pro Arg Gly 170 Arg Arg Gln Lys Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile 185 Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro 215 Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser 230 235 Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile 245 250 Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe 265 Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly 275 Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala 315 Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu 325 Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His 345

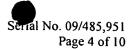


Val Gln Thr

355

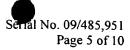


<210> 3 <211> 96 <212> DNA <213> Homo sapiens <400> 3 aacccccgca cagtccctgt tcagcctgcc ttctccacgg tgccgttctc ccagcctgtc 60 96 tgtttcccac ccaggcccag ggggcgcaga caaaaa <210> 4 <211> 1065 <212> DNA <213> Homo sapiens <400> 4 atggccttca gcggttccca ggctccctac ctgagtccag ctgtcccctt ttctgggact 60 attcaaggag gtctccagga cggacttcag atcactgtca atgggaccgt tctcagctcc 120 agtggaacca ggtttgctgt gaactttcag actggcttca gtggaaatga cattgccttc 180 cacttcaacc ctcggtttga agatggaggg tacgtggtgt gcaacacgag gcagaacgga 240 agctgggggc ccgaggagag gaagacacac atgcctttcc agaaggggat gccctttgac 300 ctctgcttcc tggtgcagag ctcagatttc aaggtgatgg tgaacgggat cctcttcgtg 360 cagtacttcc accgcgtgcc cttccaccgt gtggacacca tctccgtcaa tggctctgtg 420 cagetyteet acateagett ceagaaceee egeacagtee etgtteagee tgeettetee 480 acggtgccgt tctcccagcc tgtctgtttc ccacccaggc ccagggggcg cagacaaaaa 540 cctcccggcg tgtggcctgc caacccggct cccattaccc agacagtcat ccacacagtg 600 cagagogoco otggacagat gttototact coogcoatoo cacotatgat gtacococac 660 cccgcctatc cgatgccttt catcaccacc attctgggag ggctgtaccc atccaagtcc 720 atcetectgt caggeactgt cetgeecagt geteagaggt tecacateaa eetgtgetet 780 gggaaccaca tegeetteea eetgaaceee egttttgatg agaatgetgt ggteegeaae 840 acccagateg acaacteetg ggggtetgag gagegaagte tgeecegaaa aatgeeette 900 gtccgtggcc agagettete agtgtggate ttgtgtgaag etcaetgeet caaggtggee 960 gtggatggtc agcacctgtt tgaatactac catcgcctga ggaacctgcc caccatcaac 1020 1065 agactggaag tggggggga catccagctg acccatgtgc agaca



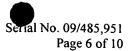
<210> 5 <211> 1725 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (82)..(1146) <400> 5 tttctttgtt aagtcgttcc ctctacaaag gacttcctag tgggtgtgaa aggcagcggt 60 ggccacagag gcggcggaga g atg gcc ttc agc ggt tcc cag gct ccc tac Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr ctg agt cca gct gtc ccc ttt tct ggg act att caa gga ggt ctc cag Leu Ser Pro Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln 15 gac gga ctt cag atc act gtc aat ggg acc gtt ctc agc tcc agt gga 207 Asp Gly Leu Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Gly acc agg ttt gct gtg aac ttt cag act ggc ttc agt gga aat gac att 255 Thr Arg Phe Ala Val Asn Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile 50 gcc ttc cac ttc aac cct cgg ttt gaa gat gga ggg tac gtg gtg tgc 303 Ala Phe His Phe Asn Pro Arg Phe Glu Asp Gly Gly Tyr Val Val Cys 60 351 aac acg agg cag aac gga agc tgg ggg ccc gag gag agg aag aca cac Asn Thr Arg Gln Asn Gly Ser Trp Gly Pro Glu Glu Arg Lys Thr His 75 atg cct ttc cag aag ggg atg ccc ttt gac ctc tgc ttc ctg gtg cag Met Pro Phe Gln Lys Gly Met Pro Phe Asp Leu Cys Phe Leu Val Gln age tea gat tte aag gtg atg gtg aac ggg ate ete tte gtg eag tae 447 Ser Ser Asp Phe Lys Val Met Val Asn Gly Ile Leu Phe Val Gln Tyr 110 tto cac ege gtg ece tto cac egt gtg gac ace ate tee gte aat gge Phe His Arg Val Pro Phe His Arg Val Asp Thr Ile Ser Val Asn Gly 125 130 tot gtg cag ctg too tac atc ago tto cag aac ccc cgc aca gto cct Ser Val Gln Leu Ser Tyr Ile Ser Phe Gln Asn Pro Arg Thr Val Pro 145 591 gtt cag cct gcc ttc tcc acg gtg ccg ttc tcc cag cct gtc tgt ttc Val Gln Pro Ala Phe Ser Thr Val Pro Phe Ser Gln Pro Val Cys Phe cca ccc agg ccc agg ggg cgc aga caa aaa cct ccc ggc gtg tgg cct





Pro	Pro	Arg	Pro	Arg 175	Gly	Arg	Arg	Gln	Lys 180	Pro	Pro	Gly	Val	Trp 185	Pro	
-		_	_				_		-					cag Gln	-	687
_			_	_					-				_	atg Met		735
			-		_	_							_	gga Gly		783
_				_				_				-	_	ccc Pro	_	831
_	_						_	-						gcc Ala 265		879
	_			-		_			_		-	_		acc Thr	_	927
								-					_	aaa Lys	_	975
		-	_		_	_						_	_	gaa Glu	_	1023
	-		_		_		-		_		_		-	tac Tyr		1071
														999 Gly 345		1119
							cag Gln		tago	gegge	ctt o	cctg	gccci	tg		1166
ggg	ccgg	ggg (ctgg	ggtg	tg gg	ggca	gtct	g ggt	cct	ctca	tcat	ccc	cac	ttcc	caggcc	1226
cago	cctt	cc a	aacc	ctgc	ct g	ggato	ctgg	g ctt	taat	gca	gag	gccat	igt (cctt	gtctgg	1286
tcci	gctt	ct (ggcta	acago	cc ad	ccct	ggaad	c gga	agaaq	ggca	gct	gacg	ggg a	attgo	ccttcc	1346
tca	gccg	cag (cagca	acct	gg gg	gctc	cagct	t gct	ggaa	atcc	taco	catco	cca (ggag	gcaggc	1406
acagccaggg agaggggagg agtgggcagt gaagatgaag ccccatgctc agtcccctcc 1												1466				





catececae geageteeae eccagteea ageeaeeage tgtetgetee tggtgggagg 1526
tggceteete ageeeeteet etetgaeett taaceteaet eteaeettge acegtgeaee 1586
aaceetteae eccteetgga aageaggeet gatggettee eactggeete eaceaeetga 1646
ceagagtgtt etetteagag gaetggetee ttteeeagtg teettaaaat aaagaaatga 1706
aaatgettgt tggeaeatt 1725



<210> 6 <211> 355 <212> PRT <213> Homo sanian

<213> Homo sapiens

<400> 6
Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro Ala Val Pro
1 5 10 15

Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu Gln Ile Thr 20 25 30

Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn 35 40 45

Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro 50 55 60

Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly 65 70 75 80

Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly $$85\,$, $$90\,$

Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val 100 105 110

Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe 115 120 125

His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr 130 135 140

Ile Ser Phe Gln Asn Pro Arg Thr Val Pro Val Gln Pro Ala Phe Ser 145 150 155 160

Thr Val Pro Phe Ser Gln Pro Val Cys Phe Pro Pro Arg Pro Arg Gly
165 170 175

Arg Arg Gln Lys Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile 180 185 190

Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe 195 200 205

Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro

210 215 220 Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser 230 235 Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile 250 Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe 265 Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly 275 280 Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala 315 Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu 330 325 Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His 345 Val Gln Thr 355 <210> 7 <211> 322 <212> PRT <213> Homo sapiens <400> 7 Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro 55

Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly

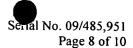
Ser Trp Gly Pro Glu Glu Arg Arg Thr His Met Pro Phe Gln Lys Met

Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val Met 105

90

110





															_				
Val	Asn	Gly 115	Ile	Leu	Phe	Val	Gln 120	Tyr	Phe	His	Arg	Val 125	Pro	Phe	His Ileannant Thr 160 Ser	A.	4		
Arg	Val 130	Asp	Thr	Ile	Phe	Val 135	Asn	Gly	Ser	Val	Gln 140	Leu	Ser	Tyr	Ile R	4/2	AT ST		
Ser 145	Phe	Gln	Pro	Pro	Gly 150	Val	Trp	Pro	Ala	Asn 155	Pro	Ala	Pro	Ile	Thr 160	12 (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	3	' O	
Gln	Thr	Val	Ile	His 165	Thr	Val [.]	Gln	Ser	Ala 170	Pro	Gly	Gln	Met	Phe 175	Ser	1900			
Thr	Pro	Ala	Ile 180	Pro	Pro	Met	Met	Tyr 185	Pro	His	Pro	Ala	Tyr 190	Pro	Met				
Pro	Phe	Ile 195	Thr	Thr	Ile	Leu	Gly 200	Gly	Leu	Tyr	Pro	Ser 205	Lys	Ser	Ile				
Leu	Leu 210	Ser	Gly	Thr	Val	Leu 215	Pro	Ser	Ala	Gln	Arg 220	Phe	His	Ile	Asn				
Leu 225	Cys	Ser	Gly	Asn	His 230	Ile	Ala	Phe	His	Leu 235	Asn	Leu	Arg	Phe	Asp 240				
Glu	Asn	Ala	Val	Val 245	Arg	Asn	Thr	Gln	Ile 250	Asp	Asn	Ser	Trp	Gly 255	Ser				
Glu	Glu	Arg	Ser 260	Leu	Pro	Arg	Lys	Met 265	Pro	Phe	Val	Arg	Gly 270	Gln	Ser				
Phe	Ser	Val 275	Trp	Ile	Leu	Cys	Gly 280	Ala	His	Cys	Leu	Lys 285	Val	Ala	Val				
Asp	Gly 290	Gln	His	Leu	Phe	Glu 295	Tyr	Tyr	His	Arg	Leu 300	Arg	Asn	Leu	Pro				
Thr 305	Ile	Asn	Arg	Leu	Glu 310	Val	Gly	Gly	Asp	Ile 315	Gln	Leu	Thr	His	Val 320				
Gln	Thr																		
<210 <211)> 8 > 35	53																	

<212> PRT

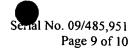
<213> Mus musculus

<400> 8

Met Ala Leu Phe Ser Ala Gln Ser Pro Tyr Ile Asn Pro Ile Ile Pro 1 5 10 15

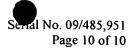
Phe Thr Gly Pro Ile Gln Gly Gly Leu Gln Glu Gly Leu Gln Val Thr 20 25 30

Leu Gln Gly Thr Thr Lys Ser Phe Ala Gln Arg Phe Val Val Asn Phe 35 40 45



Gln Asn Ser Phe Asn Gly Asn Asp Ile Ala Phe His Phe Asn Pro Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly Ser 75 Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly Met 90 Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val Met 105 Val Asn Gly Ile Leu Phe Val Gln Tyr Gln His Arg Val Pro Tyr His 120 Leu Val Asp Thr Ile Ala Val Ser Gly Cys Leu Lys Leu Ser Phe Ile Thr Phe Gln Asn Ser Ala Ala Pro Val Gln His Val Phe Ser Thr Leu Gln Phe Ser Gln Pro Val Gln Phe Pro Arg Thr Pro Lys Gly Arg Lys 165 170 Gln Lys Thr Gln Asn Phe Arg Pro Ala His Gln Ala Pro Met Ala Gln 185 Thr Thr Ile His Met Val His Ser Thr Pro Gly Gln Met Phe Ser Thr 195 200 Pro Gly Ile Pro Pro Val Val Tyr Pro Thr Pro Ala Tyr Thr Ile Pro Phe Tyr Thr Pro Ile Pro Asn Gly Leu Tyr Pro Ser Lys Ser Ile Met 235 Ile Ser Gly Asn Val Leu Pro Asp Ala Thr Arg Phe His Ile Asn Leu Arg Cys Gly Gly Asp Ile Ala Phe His Leu Asn Pro Arg Phe Asn Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asn Asn Ser Trp Gly Gln Glu 275 280 285 Glu Arg Ser Leu Leu Gly Arg Met Pro Phe Ser Arg Gly Gln Ser Phe Ser Val Trp Ile Ile Cys Glu Gly His Cys Phe Lys Val Ala Val Asn 310 315 Gly Gln His Met Cys Glu Tyr Tyr His Arg Leu Lys Asn Leu Gln Asp Ile Asn Thr Leu Glu Val Ala Gly Asp Ile Gln Leu Thr His Val Gln 340 345 350





Thr



<210> 9 <211> 28 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence:primer	
<400> 9 cgcatatggc cttcagcggt tcccaggc	28
<210> 11 <211> 30 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence:primer	
<400> 10 aacggcaccg tggagaaggc aggctgaaca	30
<210> 11 <211> 30 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence:primer	
<400> 11 aacggcaccg tggagaaggc aggctgagca	30